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Full Record**Details for HUGENEFL:X74801_AT****Full Screen**

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GeneChip Array Information

Probe Set ID X74801_at
GeneChip Array HumanGeneFL Array
Organism Common Name Human

Probe Design Information

Transcript ID X74801
Sequence Type Exemplar sequence
Representative Public ID X74801 [NCBI](#)
Target Description X74801, class B, 20 probes, 12 in X74801cds 1282-1552: 8 in reverseSequence, 1636-1837, H.sapiens Cctg mRNA for chaperonin

Genomic Alignment of Target Sequence

Assembly April 2003 (NCBI 33)
Alignment(s)

	Position	% Identity	Cytoband
chr1: 153495555-153497649 (-)	UCSC	100	q22

Overlapping Transcripts	Representative Transcript	UniGene Description	Position
	NM_005998 NCBI	chaperonin containing TCP1, subunit 3 (gamma)	chr1:153495551-153524840 (-) UCSC

Public Domain and Genome References

Gene Title chaperonin containing TCP1, subunit 3 (gamma)
Gene Symbol CCT3 [HGNC](#)
Chromosomal Location 1q23
UniGene ID Hs.1708 [NCBI](#) (FULL LENGTH)
Ensembl ENSG00000163468 [Ensembl](#)
LocusLink 7203 [NCBI](#)
SwissProt AAH06501 [EMBL-EBI](#)
P49368 [EMBL-EBI](#)
OMIM 600114 [NCBI](#)
RefSeq Protein ID NP_005989 [NCBI](#)

RefSeq	RefSeq Transcript ID	RefSeq Title
	NM_005998 <u>NCBI</u>	chaperonin containing TCP1, subunit 3 (gamma)
Functional Annotations		
	ID	Title Organism Type
	<u>ATH1-121501:246830_AT</u>	chaperonin, putative Arabidopsis Putative Ortholog
	<u>ATGENOME1:18906_AT</u>	chaperonin, putative Arabidopsis Putative Ortholog
	<u>DROSGENOME1:153982_AT</u>	Drosophila Putative Ortholog
	<u>MG-U74AV2:161238_F_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MG-U74AV2:98153_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MG-U74CV2:171548_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOE430A:1416024_X_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOE430A:1426067_X_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOE430A:1448178_A_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOE430A:1449645_S_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOE430A:1451915_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOE430A:1459987_S_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
Ortholog	<u>MU11KSUBA:C79428_RC_F_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MU11KSUBA:L20509_F_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430_2:1416024_X_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430_2:1426067_X_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430_2:1448178_A_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430_2:1449645_S_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430_2:1451915_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430_2:1459987_S_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430A_2:1416024_X_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430A_2:1426067_X_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430A_2:1448178_A_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430A_2:1449645_S_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog
	<u>MOUSE430A_2:1451915_AT</u>	chaperonin subunit 3 (gamma) Mouse Curated Ortholog

MOUSE430A_2:1459987_S_AT chaperonin subunit 3 Mouse
(gamma) Curated Ortholog

GO Biological Process (view graph)

ID	Description	Evidence	Links
6457	protein folding	traceable author statement	QuickGO AmiGO

GO Cellular Component (view graph)

ID	Description	Evidence	Links
5829	cytosol	not recorded	QuickGO AmiGO
5856	cytoskeleton	traceable author statement	QuickGO AmiGO

GO Molecular Function (view graph)

ID	Description	Evidence	Links
3754	chaperone activity	traceable author statement	QuickGO AmiGO
5524	ATP binding	inferred from electronic annotation	QuickGO AmiGO

Method	ID	Description	E-Value
blast	33873532		0.0
blast	31542292	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring complex, polypeptide 5 [Homo sapiens]	0.0

Protein Similarities

Database	ID	Description	E-Value
scop	d1a6da3	d1a6da3 SCOP:d.56.1.2: Thermosome	4.08E-25
scop	d1gmla_	d1gmla_ SCOP:c.8.5.2: Thermosome	1.01E-57
scop	d1a6da1	d1a6da1 SCOP:a.129.1.2: Thermosome	4.81E-83
pfam	cpn60_TCP1	TCP-1/cpn60 chaperonin family	5.7E-210
InterPro	IPR002423 EMBL-EBI	Chaperonin Cpn60/TCP-1	
InterPro	IPR001844 EMBL-EBI	Chaperonin Cpn60	
InterPro	IPR002194 EMBL-EBI	Chaperonin TCP-1	
InterPro	IPR008950 EMBL-EBI	GroEL-like chaperone, ATPase	

Protein Domains

Sequence

>HUGENEFL:X74801_AT
atgactggtgtggaacaatggccatacagggctgttgcccaggccctagaggtcattcct
cgtaccctgatccagaactgtggggccagcaccatccgtctacttacctcccttcgggcc
aagcacacccaggagaactgtgagacctggggtgtaaatggtgagacgggtactttggtg
gacatgaaggaactgggcataatgggagccattggctgtgaagctgcagacttataagaca
gcagtgagacggcagttctgtactgccaattgatgacatcggttcaggccacaaaag
aaaggcgatgaccagagccggcaaggcggggctcctgatgctggccaggagtgaagtcta
ggcaaggctacttcaatgcacagaaccagcagagtcctcccttttctgagccagagtgc
caggaaactgtggacgtctttgttcagaaggatcaggttggggggcagccccagtc
ctttctgtccagctcagttttccaaaagacactgacatgtaattcttctattgtaag
gtttccatttagtttgcctccgatgattaaatctaagtca

Target Sequence

Probe Sequence(5'-3')	Probe X	Probe Y	Probe Interrogation Position	Strandedness
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Probe Info	ATGACTGGTGTGGAACAATGGCCAT	60	345	1294	Antisense
	GAACAATGGCCATACAGGGCTGTTG	61	345	1306	Antisense
	CTGATCCAGAACTGTGGGGCCAGCA	62	345	1360	Antisense
	CAGAACTGTGGGGCCAGCACCATCC	63	345	1366	Antisense
	TGTGGGGCCAGCACCATCCGTCTAC	64	345	1372	Antisense
	CTGGGCATATGGGAGCCATTGGCTG	65	345	1486	Antisense
	ATATGGGAGCCATTGGCTGTGAAGC	66	345	1492	Antisense
	GAGCCATTGGCTGTGAAGCTGCAGA	67	345	1498	Antisense
	TTGGCTGTGAAGCTGCAGACTTATA	68	345	1504	Antisense
	GAGACGGCAGTTCTGCTACTGCGAA	69	345	1540	Antisense
	GCAGTTCTGCTACTGCCAATTGATG	70	345	1546	Antisense
	ATTGATGACATCGTTTCAGGCCACA	71	345	1564	Antisense
	GTGCTAGGCAAGGCTACTTCAATGC	72	345	1648	Antisense
	GGCAAGGCTACTTCAATGCACAGAA	73	345	1654	Antisense
	GCTACTTCAATGCACAGAACCAGCA	74	345	1660	Antisense
	CACAGAACCAGCAGAGTCTCCCCTT	75	345	1672	Antisense
	GAGCCAGAGTGCCAGGAACACTGTG	76	345	1702	Antisense
	CACTGACATGTAATTCTTCTCTATT	77	345	1804	Antisense
	TAGTTTGCTTCCGATGATTAAATCT	78	345	1843	Antisense
	GCTTCCGATGATTAAATCTAAGTCA	79	345	1849	Antisense

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